

# STRBase: A web based resource for STR information

Register | Log in

- Commonly Used Auto STRs
- Other Auto STRs
- X-Chromosome STRs
- Y-Chromosome STRs

### Commonly Used Auto STRs

- CSF1PO
- D10S1248
- D12S391
- D13S317
- D16S539
- D18S51
- D19S433
- D1S1656
- D21S11
- D22S1045
- D2S1338
- D2S441
- D3S1358
- D5S818
- D6S1043
- D7S820
- D8S1179
- FGA
- Penta D
- Penta E
- SE33
- TH01
- TPOX
- VWA

### Introduction

The web-based Short Tandem Repeat Database (STRBase – <https://strbase.nist.gov>) was developed in 1997 and released to the public in July of that year. The original goal of the site was to bring together information about STR systems to support the human identity community.

**Usage** - The STRBase site has evolved into a place where analysts in forensics labs verify allele information, technical leaders can find and download training information, and researchers and methods developers can search for various kinds of STR-related information. Over the years many institutions and researchers have contributed information to this resource, which continues to this day.

**Goal** - Since its inception, the design of the site has been relatively constant with minimal changes made to the underlying IT architecture. A redesign of the web-based tool is currently underway to make enhancements to the user interface. The goal is to maintain information in an accessible format while allowing the new site to be more easily sustained.

**Future** - STRBase 2.0 is currently under development and will soon be available to the public for beta testing. User feedback is greatly appreciated and will be incorporated into the development of STRBase 2.0.

### Purpose

The process of updating the Classic website started with a simple overhaul of the original site. This included adding navigation and making the site visually uniform (New Classic see below). Google analytics was also incorporated into the updated site allowing for an understanding of what pages were being utilized by the user. The pie chart in the lower left is the top 10 pages identified by views in the last year. These pages represent a variety of starting points when exploring STRBase. In early 2017, a survey was made available on the site to obtain user information and feedback about the site. This information assisted us in the design focus of STRBase 2.0.

- Improved navigation and the ability to quickly find information.
- Registration and login capabilities.
- An automated submission process for variant and tri-alleles.
- The ability to search, sort, and download information for variant and tri-alleles.
- Updating and removing out of date information to help focus the site on what users are accessing.

Some of the updated and new features are described to the left with images of the new site. Including an image of the main page in the lower right.

### Updates

#### Navigation

- The site has been reorganized to simplify the navigation.
- Information about individual STRs have been brought together in a common interface.
- Users can now quickly access locus information through the left menu on the site (expanded example to the left).
- The search box can be used to find information about key words, full and partial loci names (example below).

**Search Results:**

Search string: Penta

Loci Matches:

Locus	Genome	Chromosome	Publication	STRSeq BioProject
Penta D	GRCh38	21		PRJNA380576
Penta E	GRCh38	15		PRJNA380571

### New Features

#### Register/Login - optional

- Users will not be required to register or login to use the site
- However, a user has the option of registering and will receive update notifications as the site continues to add information.
- Additionally, registered users may request the ability to submit allele information to the site through a submission portal.
- This will simplify the submission process for contributors and streamline the process on the back end.

Register - Create a New Account

Email:  Password:

First Name:  Confirm password:

STR:

Last Name:  Base:

#### Submitting Data

A submission form will be available to users who request the ability to upload variant and tri-allelic information. The form will be easy for the user to provide the needed information to build the record (example to the right). Once submitted it will be reviewed and then made publicly available in the tables on the STRBase site.

#### Tables

- The variant and tri-alleles tables have been updated with:
- Search table contents.
- Sort columns.
- Download data - export to excel, comma-separated values, or text file types.

The tables have been simplified to focus on key information but all information is still accessible (example upper right).

#### Content

Although some content will not be included in STRBase 2.0, the old site, **which will not be maintained or updated**, will be available for a period of time at [strbase-archive.nist.gov](http://strbase-archive.nist.gov) while the transition to the new site is taking place. Additionally, after the old site is taken down the files that make up the classic site will be made available for download.

### Submit a New Variant Allele

**Submit New Variant Allele Finding**

Locus Id: **D12S391**

**Proposed interface for the submission of variant STR alleles**

Instrument/Kit: Select instrument used: ABI 3500  
Select amplification kit used: Powerplex Fusion 6C

Allele Call:

Allele Call is less than:

Allele Call is greater than:

Allele size range (If single number, place in Min and leave Max blank)

Min (bp):  Max (bp):

Is Allele Size an approximation/average?

If multiple runs, indicate number:

**Analysis Details**

Select verification/confirmation method: Re-ran original amplified product, Observation in multiple samples

Additional Notes:

Variant Allele for D1S1656

Allele Call	Size	Instrument	Amp Kit	Action
10.3	138.15	ABI 3500 XL	Powerplex ESX 16 (Fast)	<input type="checkbox"/>
11.1	140.24	ABI 3130 XL	Powerplex ESX 16 (Fast)	<input type="checkbox"/>
11.3	142.21	ABI 3500 XL	Powerplex ESX 16 (Fast)	<input type="checkbox"/>
12.1	170.64	ABI 3500	Powerplex 21	<input type="checkbox"/>
12.3	146.19	ABI 3500 XL	Powerplex ESX 16 (Fast)	<input type="checkbox"/>
12.3	172.66	ABI 3500	Powerplex 21	<input type="checkbox"/>
13.1	148.52	ABI 3130 XL	Powerplex ESX 16 (Fast)	<input type="checkbox"/>
13.3	192.5	ABI 3500	NGM Select/Detect (Express)	<input type="checkbox"/>

**STR General information page**

Variant Allele: Tri Allele Kits General Info. Search:

Export to xls Export to csv Export to txt

Chromosome Location/Allele Reference

Genome	Chromosome	Start	End	CE	Bracket Sequence
GRCh38	5	150076324	150076375	13	[ATCT]3

Cytogenetic Location: 5q22  
Sequence Pattern: [ATCT]3

Nomenclature Publication: Hammond HA, Jin L, Zheng Y, Casley CT, Chakraborty R. Evaluation of 13 short tandem repeat loci for use in personal identification applications. Am J Hum Genet. 1994 Jul;55(1):175-88. PubMed PMID: 7912887; PubMed Central PMCID: PMC1918218 (PubMed)

STRSeq BioProject: PRJNA380561

Mutation: 

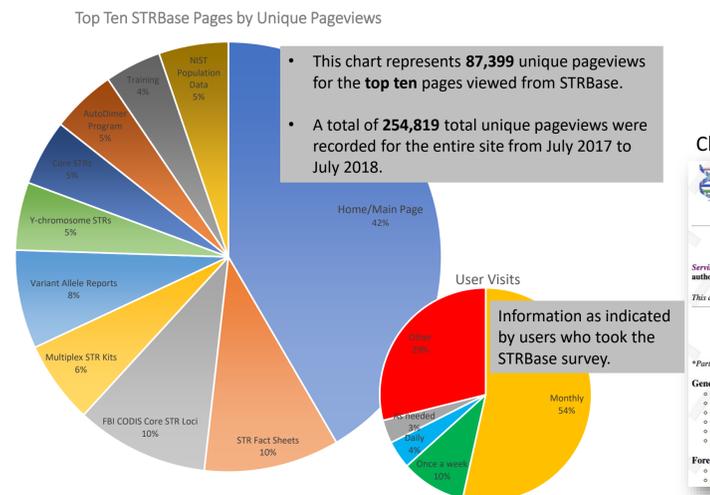
Rate	Data Source	US Source	Action
0.15%	AAB003	Table 14.5 of Butler, 2015	<input type="button" value="Q"/>

Core Sets including this Locus: CODIS Loci, US Core Loci

Alternative Names: CSF1PO

Historic Names: CSF

- Other Auto STRs
- X-Chromosome STRs
- Y-Chromosome STRs



### Classic (1997 to 2017)

**Short Tandem Repeat DNA Internet DataBase**

NIST Standard Reference Database SRD 130 [Recent Updates]

Serving the forensic DNA and human identity testing communities for over 10 years... These data are intended to benefit research and application of short tandem repeat DNA markers to human identity testing. The authors are solely responsible for the information herein.

This database has been accessed >500,000 times since 10/02/97.

Created by John M. Butler and Dennis J. Reader (NIST Biomedical Science Division) with invaluable help from Jan Redman, Christian Rutberg and Michael Tang. Site creator's curriculum vitae available using link above.

\*Partial support for the design and maintenance of this website is being provided by The National Institute of Justice through the NIST Law Enforcement Standards Office.\*

**General Information**

- Purpose of STRBase/SAR 2001 Paper describing STRBase/Overview Presentation
- Publications and Presentations from NIST Human Identity Project Team
- NIE-Funded Projects
- Training Materials
- Links to other web sites
- Glossary of commonly used terms

**Forensic STR Information**

- STRBase - Brief Introduction to STR
- Core Loci: FBI CODIS Core STR Loci and European Core Loci

The evolution of the websites main page. From the original main page, Classic (left) to the updated main page, New classic (middle) and the redesigned main page of STRBase 2.0 (right).

### New Classic (2017 to 2019)

**STRBase (SRD-130)**

NIST Standard Reference Database SRD 130 [Recent Updates on 08/16/2018]

Serving the forensic DNA and human identity testing communities for 20 years... These data are intended to benefit research and application of short tandem repeat DNA markers to human identity testing. The authors are solely responsible for the information herein.

This database has been accessed >500,000 times since 10/02/97.

Created by John M. Butler and Dennis J. Reader (NIST) with invaluable help from Jan Redman, Christian Rutberg and Michael Tang. Site creator's curriculum vitae available using link above.

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**Beta release STRBase 2.0**

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### STRBase 2.0 (fall 2018 beta release www.strbase-b.nist.gov)

**STRBase 2.0 (Short Tandem Repeat DataBase)**

Commonly Used Auto STRs

Other Auto STRs

X-Chromosome STRs

Y-Chromosome STRs

**Introduction**

STRBase is a resource for Short Tandem Repeat and other human identification markers. Within this site, users can manage, search, and download locus information such as reported variant alleles, tri-alleles, and general information including genomic coordinates, allele size ranges, sequence motifs. Information is also available by kit or core set and registered users can upload newly observed length-based variant alleles and receive alerts of new information on pages of interest.

Additionally, STRBase hosts content produced by NIST Applied Genetics: publications, presentations, population data, sample data sets, and information regarding Standard Reference Materials of interest to the Forensic DNA community. STR data produced via next generation sequencing is cataloged separately in the STRSeq BioProject at NCBI, with sequence-specific tools and resources forthcoming at [strseq.nist.gov/](http://strseq.nist.gov/).

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